

Gencore version 5.1.6  
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ON protein - protein search, using sw model

Run On: June 3, 2003, 14:59:46 : Search time 70 Seconds  
(Without alignments)  
454,956 Million cell updates/sec

Title: US-09-887-784-4

Perfect score: 1274  
Sequence: 1 WPKSEEEFTGVPVILFED . . . . . VLGFTYAAGITGMDLYK 239

Scoring table: BLOSUM62  
Gapext 10.0 Gapext 0.5

Searched: 908470 seeds, 13320620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 9  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Summaries

Listing first 45

Database: A\_GeneSeq\_101002,\*

1: STD5/939dat/1/geneseed/geneseed/emb|/AAl1980 DAT-\*  
2: STD5/939dat/1/geneseed/geneseed/emb|/AAl1981 DAT-\*  
3: STD5/939dat/1/geneseed/geneseed/emb|/AAl1982 DAT-\*  
4: STD5/939dat/1/geneseed/geneseed/emb|/AAl1983 DAT-\*  
5: STD5/939dat/1/geneseed/geneseed/emb|/AAl1984 DAT-\*  
6: STD5/939dat/1/geneseed/geneseed/emb|/AAl1985 DAT-\*  
7: STD5/939dat/1/geneseed/geneseed/emb|/AAl1986 DAT-\*  
8: STD5/939dat/1/geneseed/geneseed/emb|/AAl1987 DAT-\*  
9: STD5/939dat/1/geneseed/geneseed/emb|/AAl1988 DAT-\*  
10: STD5/939dat/1/geneseed/geneseed/emb|/AAl1989 DAT-\*  
11: STD5/939dat/1/geneseed/geneseed/emb|/AAl1990 DAT-\*  
12: STD5/939dat/1/geneseed/geneseed/emb|/AAl1991 DAT-\*  
13: STD5/939dat/1/geneseed/geneseed/emb|/AAl1992 DAT-\*  
14: STD5/939dat/1/geneseed/geneseed/emb|/AAl1993 DAT-\*  
15: STD5/939dat/1/geneseed/geneseed/emb|/AAl1994 DAT-\*  
16: STD5/939dat/1/geneseed/geneseed/emb|/AAl1995 DAT-\*  
17: STD5/939dat/1/geneseed/geneseed/emb|/AAl1996 DAT-\*  
18: STD5/939dat/1/geneseed/geneseed/emb|/AAl1997 DAT-\*  
19: STD5/939dat/1/geneseed/geneseed/emb|/AAl1998 DAT-\*  
20: STD5/939dat/1/geneseed/geneseed/emb|/AAl1999 DAT-\*  
21: STD5/939dat/1/geneseed/geneseed/emb|/AAl2000 DAT-\*  
22: STD5/939dat/1/geneseed/geneseed/emb|/AAl2001 DAT-\*  
23: STD5/939dat/1/geneseed/geneseed/emb|/AAl2002 DAT-\*

pred. No. is the number of results produced by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1274	100.0	239	23	AAl17518	Enhanced F41-E222
2	1274	100.0	893	22	AAl65181	Amino acid sequence
3	1274	100.0	1122	22	AAl65182	Amino acid sequence
4	1266	99.4	239	23	AAl17517	Enhanced F41-J41
5	1263	99.1	239	21	AAl22082	Enhanced Green Flu
6	1263	99.1	239	21	AAl79584	EGFP signal domain
7	1263	99.1	239	21	AAl51449	Amino acid sequence
8	1263	99.1	239	22	AAl31771	Amino acid sequence
9	1263	99.1	239	22	AAl50304	Jellyfish GFP muta
10	1263	99.1	239	22	AAl55930	A. Victoria green

A. victoria green	AAAG66198	239	23	AAG66198	A. victoria green
Jellyfish green fl	AAG68119	248	23	AAAG68119	Jellyfish green fl
Biomembrane permea	AAAG9904	259	23	AAAG9904	Biomembrane permea
Wild-type Green fl	AAAG9751	265	20	AAAG9751	Wild-type Green fl
Biomembrane permea	AAAG9903	268	23	AAAG9903	Biomembrane permea
Biomembrane permea	AAAG9902	270	23	AAAG9902	Biomembrane permea
Biomembrane permea	AAAG9900	272	23	AAAG9900	Biomembrane permea
Biomembrane permea	AAAG9901	273	23	AAAG9901	Biomembrane permea
Green fluorescent	AAAG9902	280	23	AAAG9902	EGFP-MOD42-461 f
EGFP-MOD42-461 f	AAAG95042	281	21	AAAG95042	EGFP-MOD42-461 f
EGFP-DRM annexin I	AAU10888	281	23	AAU10888	EGFP-DRM annexin I
Caspase-3 like	AAU22660	284	21	AAU22660	Caspase-3 like
Human ANP/ Green fl	AAU79538	284	21	AAU79538	Human ANP/ Green fl
EGFP/DRM fusion pr	AAU42181	308	20	AAU42181	EGFP/DRM fusion pr
EGFP mutant	AAU54359	323	21	AAU54359	EGFP mutant
T. maritima HU/EGF	AAU86137	328	22	AAU86137	T. maritima HU/EGF
EGFP/DRM fusion pr	AAU42179	336	20	AAU42179	EGFP/DRM fusion pr
EGFP/DRM fusion pr	AAU42175	339	20	AAU42175	EGFP/DRM fusion pr
Green fluorescent	AAU55356	344	20	AAU55356	Green fluorescent
IL-1 alpha propept	AAU22336	344	19	AAU22336	IL-1 alpha propept
Alpha actinin acti	AAU6161	344	19	AAU6161	Alpha actinin acti
CDB2-green fluores	AAU50289	386	23	AAU50289	CDB2-green fluores
Green fluorescent	AAU50289	391	23	AAU50289	Green fluorescent
EGFP/DRM fusion pr	AAU22778	397	20	AAU22778	EGFP/DRM fusion pr
EGFP/DRM fusion pr	AAU21776	403	20	AAU21776	EGFP/DRM fusion pr
EGFP/DRM fusion pr	AAU21775	403	20	AAU21775	EGFP/DRM fusion pr
Amino acid sequenc	AAU50116	442	19	AAU50116	Amino acid sequenc
Er2'-green fluores	AAU50116	442	19	AAU50116	Er2'-green fluores
Antino acid sequenc	AAU50116	604	22	AAU50116	Antino acid sequenc

### ALIGNMENTS

RESULT 1  
AAE17518 standard: protein: 239 AA.

XX

AC

AAE17518;

DT 22-APR-2002 (first entry)

XX

DE Enhanced F61-E2226 Jellyfish green fluorescent protein mutant.

XX

KW Jellyfish; green fluorescent protein; GFP; protein redistribution;

KW cellular function; genetic reporter; mutant; Stoke's shift; mutant.

XX

OS Synthetic.

OS Aequorea victoria.

XX

PH Key

PT Misc-difference 65

PT Misc-difference 233

PT Misc-difference 222

PT corresponds to position 222 in the wild type protein\*

PT location/qualifiers

PT note\* Wild type Phe substituted with Leu; This

PT corresponds to position 64 in the wild type protein\*

PT note\* Wild type Glu substituted with Gly; This

PT corresponds to position 222 in the wild type protein\*

A. Victoria green

Jellyfish GFP muta

A. Victoria green

KW autoimmune; KW ischemic; KW osteopathic; GFP: green fluorescent protein; KW fusion protein.

PRR	10-MAY-2001	2001US-290170P.
PA	XX	(B101)- BIOMAGE AS.
PA	PA	
PI	BIJORN SP.	Pagliaro L., Thastrup O.
WPI:	2002-08224/13.	
DR	DR	N-PSDB; AAD8163.
XX	XX	
PP	PP	Novel fluorescent protein in in vitro assay for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution, has a green fluorescent protein with F64L and E22G mutation
PT	PT	
DR	DR	
XX	XX	
PS	PS	Claim 9; Page 37; 41pp; English.
CC	CC	The invention relates to a fluorescent protein derived from green fluorescent protein (GFP) or its analogue. The GFP containing mutations at F64L and E22G has a bigger compared to other GFP's making it very suitable for high throughput screening due to better resolution. The fluorescent protein is useful in in vitro assays for measuring protein kinase activity or dephosphorylation activity, or for measuring protein redistribution. The fluorescent protein is useful in studying cellular functions in living cells; as protein tags in transgenic animals, living and fixed cells; organelle tags; as marker and generic reporter. The fluorescent protein is also useful as a cell or organelle integrity marker, a marker for changes in cell morphology, as transfection marker, and as a marker to be used in combination with fluorescence activated cell sorting (FACS). The novel proteins can also be used as reporters to monitor live or dead biomass of organisms, such as fungi. The fluorescent protein is also useful as markers in transcriptional and translational fusions for performing transposon vector mutagenesis and as a reporter for bacterial detection. The fluorescent protein are useful for screening promoters and encoding the fluorescent protein are useful for designing diagnostic tool. The sequence is a DNA sequence for designing F64L-E22G jellyfish green fluorescent protein (GFP) mutant.
SO	SO	Sequence 239 AA;
Query	Query	Score: 100.0%; Length: 239;
Best Local Similarity	100.0%	Score: 1274; Length: 23;
Matches	239;	Score: 100.0%; Length: 23;
Conservative	0;	Score: 100.0%; Length: 23;
Mismatches	0;	Score: 100.0%; Length: 23;
Indels	0;	Score: 100.0%; Length: 23;
Gaps	0;	Score: 100.0%; Length: 23;
QY	QY	1 MVSKEELFTGVPLIVELDGUNHSHPSVSEGEGATGTLAICPTOKLIVVHPPT 60
Db	Db	1 MVSKEELFTGVPLIVELDGUNHSHPSVSEGEGATGTLAICPTOKLIVVHPPT 60
QY	QY	61 LTVLTLSKGQCSRYSPVPHKQIDFKEKAPESVYQESTFFDQGNYKTRAEVKPECDTL 120
Db	Db	61 LTVLTLSKGQCSRYSPVPHKQIDFKEKAPESVYQESTFFDQGNYKTRAEVKPECDTL 120
QY	QY	121 VRIELKGIDFENGTLAHLKLEYNIVSINYINNIAIDQKNGKVNINRHEEDGYSQLA 180
Db	Db	121 VRIELKGIDFENGTLAHLKLEYNIVSINYINNIAIDQKNGKVNINRHEEDGYSQLA 180
QY	QY	181 DHYQONTIPQIDGPSPVLPFLDNYHLSQSALSKDPKRHDAYLGFYTQGTTGMDELYK 239
Db	Db	181 DHYQONTIPQIDGPSPVLPFLDNYHLSQSALSKDPKRHDAYLGFYTQGTTGMDELYK 239
RESULT 2		
AA6565781.		
AA6565781.	standard;	Protein; 893 AA.
XX	XX	
TD	TD	
AC	AC	
AX	AX	
DT	DT	
DE	DE	
AX	AX	
Q	Q	
RA	RA	
07-JAN-2002	(first entry)	
Amino acid sequence of HSPDE4A1-B22G fusion protein.		
PDB4: central nervous system; antiinflammatory; cytoplastic; nootropic;		

ID	AAC65782	standard; Protein; 1132 AA.	Db	1014 VNRIELKGKDFKEDGNLIGHKLEYNNSHNYIMADKORGKIVNFKIRHIEDGSVQLA 1073
XX	XX		Qy	181 DHYQNTREIDGDPVLPDNPYHLSLTSQALSKPNEKRDHNVLGVFTAGITLGHDLEYK 239
AC	AC		Db	1074 DHYQNTREIDGDPVLPDNPYHLSLTSQALSKPNEKRDHNVLGVFTAGITLGHDLEYK 1132
XX	DT	07-JAN-2002 (first entry)		
XX	DE	Amino acid sequence of HSPD4A4-E222G fusion protein.		
XX	XX	PDA4; central nervous system; antiinflammatory; cyrostatic; nootropic;		
XX	XX	autoimmune; ischamic; osteopathic; GFP; green fluorescent protein;		
XX	XX	fusion protein.		
XX	XX	Human sapiens		
OS	OS	Aequorea victoria.		
XM	XM	W0200179526-A2.		
PN	PN	2001WO179526-A2.		
XX	XX	25-OCT-2001.		
PD	PD	11-APR-2001; 2001WO-DK00264.		
XX	XX	PR 17-APR-2000; 2000DK-0000651.		
PR	PR	29-MAY-2000; 2000DK-0000849.		
XX	XX	PA (BIO) - BIOIMAGE AS.		
PA	PA	PI Terry BR, Scudder KM, Bjorn SP, Thastrup O, Almholz DC;		
PI	PI	Preestgaard M;		
XX	XX	DR WP: 2001-011727-70,		
DR	DR	NPDBP, AAC65653.		
XX	XX	P1 Determining if a compound is a dislocator of PDE4 for identifying		
P1	P1	compounds for treating CNS and inflammatory disease comprises		
PT	PT	Identifying compounds which remove PDE4 spots		
XX	XX	Example 1; Page 162-167- 160pp; English.		
XX	XX	CC The invention relates to determining, if a compound, is a dislocator of		
CC	CC	PDE4. The method comprising testing if the compound removes PDE4 spots,		
CC	CC	which may optionally be induced by a Ro514-1118 reference compound,		
CC	CC	and testing if it inhibits the catalytic activity of the PDE4, where the		
CC	CC	compound is a dislocator of PDE4, if it removes PDE4 spots and if it does		
CC	CC	not inhibit the catalytic activity of PDE4. The method is useful for		
CC	CC	Identifying compounds useful for the treatment of diseases of the central		
CC	CC	nerve system, such as depression and for the treatment of inflammatory		
CC	CC	diseases such as joint, inflammatory bowel		
CC	CC	respiratory diseases, chronic obstructive pulmonary disease,		
CC	CC	chronic bronchitis, pulmonary emphysema,		
CC	CC	endothelial shock, toxic shock syndrome, systemic lupus erythematosus,		
CC	CC	psoriasis, bone resorption diseases, reperfusion injury, cancer and HIV		
CC	CC	infection. The use of a reagent that can mimic or reverse the effect of		
CC	CC	the compound with affinity for the catalytic site on intracellular		
CC	CC	distribution of the PDE4 for the preparation of a medicament. The present		
CC	CC	sequence represents the amino acid sequence of a HSPD4A4-E222G fusion		
CC	CC	protein.		
XX	XX	Sequence 1132 AA:		
Qy	Qy	Query Match 100.0%; Score 1274; DB 22; Length 1132;		
Best Local Similarity 100.0%; Ped. No. 2 6-122;				
Matches 239; Conservative 0; Mismatches 0; Gaps 0;				
Qy	1	MYSKGEIPLGQVPLVLDQDNGKRSVSGGEQDATYKULITFCITGKLPWPR 60		
894	894	MYSKGEIPLGQVPLVLDQDNGKRSVSGGEQDATYKULITFCITGKLPWPR 953		
Qy	61	LYTTLTSYCVCFSPRDPDMDKORFPPSAMPGTYQSRIFTKFDQGKTRAVFKEGDIL 120		
DB	954	LYTTLTSYCVCFSPRDPDMDKORFPPSAMPGTYQSRIFTKFDQGKTRAVFKEGDIL 1013		
Qy	121	VNRIELKGKDFKEDGNLIGHKLEYNNSHNYIMADKORGKIVNFKIRHIEDGSVQLA 180		

CC diagnostic tool. The present sequence is enhanced F64L jellyfish green  
 CC fluorescent protein (GFP) mutant.

XX

SO

Sequence 239 AA:

Query Match 99.4%; Score 1266; DB 23; Length 239;

Best Local Similarity 99.6%; Pred. No. 1.Re-122;

Mismatches 0; Gaps 0;

Matches 23; Conservative 0; Indels 0;

Score 1266; DB 23; Length 239;

Qy 1 MYSKEELFTGVPILVEDQDYNHKPSVSGEGDATYCKULFCTGKLPVPPW 60

Db 1 MYSKEELFTGVPILVEDQDYNHKPSVSGEGDATYCKULFCTGKLPVPPW 60

Qy 61 LYTTLSYQOCFSRYPDMDKQHDFKSAMPGTYQERITFKDQGKTYRAEYKFGDNL 120

Db 61 LYTTLSYQOCFSRYPDMDKQHDFKSAMPGTYQERITFKDQGKTYRAEYKFGDNL 120

Qy 121 VRILRLQDFKDNLIGHKLYNNHVNIMADKORNKIVNPKRKRHNDGVSOLA 180

Db 121 VRILRLQDFKDNLIGHKLYNNHVNIMADKORNKIVNPKRKRHNDGVSOLA 180

Qy 181 DHYQONTPIGEVLPNHYLTSOSALSKDPEKRDINVLGLATGFLDLYK 239

Db 181 DHYQONTPIGEVLPNHYLTSOSALSKDPEKRDINVLGLATGFLDLYK 239

XX



RESULT 8  
AAB31171 standard; protein: 239 AA.  
ID AAB31171;  
XX  
AC AAB31171;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Amino acid sequence of a green fluorescent protein (GFP).  
XX  
Growth rate; death rate; reporter gene; luminescent protein;  
fluorescent product; luciferase; green fluorescent protein; GFP.  
XX  
KW Aequorea victoria; jellyfish; fluorescent protein indicator;  
green fluorescent protein; GFP; linker moiety; sensor;  
calmodulin-binding domain; mutant; mutant; mutant.  
XX  
OS Aequorea victoria.  
XX  
PN WO200075367-A1.  
XX  
PD 14-DEC-2000.  
XX  
PP 07-JUN-2000; 2000MO-F100507.  
XX  
PR 07-JUN-1999; 99P1-0001296.  
XX  
PA (LILJUS E.  
(VIRTA M.)  
XX  
PI LILJUS E, Virta M;  
XX  
DB WO1-061727/07.  
DR N P SDB; AAC6694.  
XX  
PR Assessing growth and death rates of a micro-organism in a desired environment by introducing 2 reporter genes encoding luminescent and fluorescent products and detecting luminescent fluorescence -  
XX  
PS Disclosure: Page 27; 32PP; English.  
XX  
CC The specification describes a method for assessing the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two reporter genes encoding luminescent and/or fluorescent products into the micro-organism, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The present sequence represents a green fluorescent protein (GFP), and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is used in the method of the invention.  
XX  
Sequence 239 AA:

RESULT 9  
AAB30804 standard; protein: 239 AA.  
ID AAB30804;  
XX  
AC AAB30804;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Jellyfish GFP mutant EGFP.  
XX  
Aequorea victoria; jellyfish; fluorescent protein indicator;  
KW green fluorescent protein; GFP; linker moiety; sensor;  
calmodulin-binding domain; mutant; mutant; mutant.  
XX  
OS Aequorea victoria.  
XX  
PN WO200071565-A2.  
XX  
PD 30-NOV-2000.  
XX  
PP 17-MAY-2000; 2000WO-0511684.  
XX  
PR 21-MAY-1999; 99US-031619.  
PR 21-MAY-1999; 99US-031620.  
XX  
(REGC ) UNITY CALIFORNIA.  
XX  
TSien RY, Baird GA;  
XX  
WPI: 2001-032017/04.  
DR N P SDB; AAC50486.  
XX  
PR Novel fluorescent protein comprising a sensor protein inserted into a polypeptide that is responsive to a chemical, biological, electrical, or physical parameter, and a fluorescent protein functional group. The sensor polypeptide is operatively inserted into the fluorescent polypeptide. The fluorescent indicator is useful for detecting the presence of a response-inducing member in a sample. The method involves contacting the sample with the indicator and detecting a change in fluorescence, in which a change is indicative of the effect of the parameter on the sensor polypeptide. The novel fluorescent proteins are advantageous due to their reduced size as compared to the FRET (fluorescence resonance energy transfer)-based sensors.  
XX  
Sequence 239 AA:

Query Match 99.1%; Score 1263; DB 22; Length 239;  
Best Local Similarity 99.1%; Prod. No. 3.9e-12; Gaps 0;  
Matches 23; Conservative 23; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MVSKEBEFTGPVPLIVELDDYDNGAKTSVSGEEDATYKTLFICITGKLPWPWT 60  
1 MVSKEBEFTGPVPLIVELDDYDNGAKTSVSGEEDATYKTLFICITGKLPWPWT 60  
DB 61 LPTTISKYCGCERYDHNKCPFYSAMPCKYVQRTPTKDKCHYKRAKVKPGSL 120  
61 LPTTISKYCGCERYDHNKCPFYSAMPCKYVQRTPTKDKCHYKRAKVKPGSL 120  
QY 61 LPTTISKYCGCERYDHNKCPFYSAMPCKYVQRTPTKDKCHYKRAKVKPGSL 120  
61 LPTTISKYCGCERYDHNKCPFYSAMPCKYVQRTPTKDKCHYKRAKVKPGSL 120  
DB 61 LPTTISKYCGCERYDHNKCPFYSAMPCKYVQRTPTKDKCHYKRAKVKPGSL 120  
61 LPTTISKYCGCERYDHNKCPFYSAMPCKYVQRTPTKDKCHYKRAKVKPGSL 120  
QY 121 VNRTEKLGIDPKEDGAGLGHLEKLYNNNSHNTYMAKOKNGTKYNEKFRHNTEDGSVLA 180  
121 VNRTEKLGIDPKEDGAGLGHLEKLYNNNSHNTYMAKOKNGTKYNEKFRHNTEDGSVLA 180  
DB 121 VNRTEKLGIDPKEDGAGLGHLEKLYNNNSHNTYMAKOKNGTKYNEKFRHNTEDGSVLA 180  
QY 181 DHYQNTPQGQGPVLPDNTLPSQASLKSQPKRDNWLLGPYAACTLGNDLYK 239  
181 DHYQNTPQGQGPVLPDNTLPSQASLKSQPKRDNWLLGPYAACTLGNDLYK 239  
DB





Qy	61 LYTTISGVQCFSPRYDPHMKQHDFKFSAMPESVYQERTIFFKDGKNTKRAVEKEPDYL 120      :     :     :     :     :     :     :     :     :     :     :     : 61 LYTTISGVQCFSPRYDPHMKQHDFKFSAMPESVYQERTIFFKDGKNTKRAVEKEPDYL 120	Db	61 LYTTISGVQCFSPRYDPHMKQHDFKFSAMPESVYQERTIFFKDGKNTKRAVEKEPDYL 120 121 VNRTEKIDFEDQDNTGKLEKLYNTSHNYYTIAQDQNGKVNFKIRHNEEDSYLA 180      :     :     :     :     :     :     :     :     :     :     : 121 VNRTEKIDFEDQDNTGKLEKLYNTSHNYYTIAQDQNGKVNFKIRHNEEDSYLA 180	
Qy	121 VNRTEKIDFEDQDNTGKLEKLYNTSHNYYTIAQDQNGKVNFKIRHNEEDSYLA 180      :     :     :     :     :     :     :     :     :     :     : 121 VNRTEKIDFEDQDNTGKLEKLYNTSHNYYTIAQDQNGKVNFKIRHNEEDSYLA 180	Db	121 VNRTEKIDFEDQDNTGKLEKLYNTSHNYYTIAQDQNGKVNFKIRHNEEDSYLA 180 181 DHYQNTPIGDVLPNHNNTYDOSALSKPNEKDINYLLEPFTAGITLGDELYK 239      :     :     :     :     :     :     :     :     :     : 181 DHYQNTPIGDVLPNHNNTYDOSALSKPNEKDINYLLEPFTAGITLGDELYK 239	
Qy	181 DHYQNTPIGDVLPNHNNTYDOSALSKPNEKDINYLLEPFTAGITLGDELYK 239      :     :     :     :     :     :     :     :     : 181 DHYQNTPIGDVLPNHNNTYDOSALSKPNEKDINYLLEPFTAGITLGDELYK 239	Db	181 DHYQNTPIGDVLPNHNNTYDOSALSKPNEKDINYLLEPFTAGITLGDELYK 239 RESULT 15 ID AAWS7451 standard; Protein: 265 AA. XX AAWS7451;	
Qy	AAW93604 standard; Protein: 259 AA. XX AAW93604 AC AC XX XX	Db	19-MN-1999 (first entry) DT 07-OCT-2002 (first entry) XX DE Biomembrane permeable compound associated EGFP-Histidine tag protein. XX KW Biomembrane permeating signal sequence; nucleic-acid transfer signal. KW post-synapse transfer signal sequence; biomembrane-permeable compound; KW PCR primer; ss; enhanced green fluorescent Protein; EGFP; His tag; KW histidine tag. XX OS Synthetic.	
Qy	JP2002152288-A. XX PD 28-MAY-2002. XX PF 24-NOV-2000; 2000JP-0358442. XX PR 24-NOV-2000; 2000JP-0358442. XX PA (MATS) MATSUI, I. PA (MATS) MATSUHITA, M. XX WP: 2002-552745/59. DR XX PT Compound for introducing a substance to a specific site in a cell, a vector - PT Compound for introducing a substance to a specific site in a cell, a vector - PT PAK Inhibitor; a transcription inhibitor, a vector - XX PS Example 1; Page 16, 25pp; Japanese.	Db	04-JUN-1998: 98WO-FR01136. XX PR 05-JUN-1997: 97FR-0006577. XX PA (CNRS ) CNRS CENT NAT RECH SCI. PT Alix P, Galzi JL; PT XX PR 1999-142415/12. DR N PDB; RAX1606. XX PT Detecting non-covalent interactions between target protein and PT ligand - using green fluorescent protein as energy transfer label PT for reactants, used to, e.g. identify potential therapeutics binding PT to G protein-coupled receptors XX PS Disclosure: Fig 1; 103EP; French. XX CC The present sequence represents wild-type green fluorescent protein CC (GFP). The specification describes the use of GFP, or its fluorescent CC variants and derivatives, for detecting and quantifying non-covalent CC interactions between a target protein, genetically labelled by GFP, CC and a ligand within a group that can absorb light emitted from CC GFP or is a fluorescent resonance substance. The method is based on fluorescent CC energy transfer between GFP and the group, with the fluorescence CC substance being excited by light emitted from GFP or emitting at CC the GFP excitation wavelength. The labelled reagents are especially CC used to assess interaction between a G protein-coupled receptor and a CC G protein, particularly to identify agents interacting reversibly at CC the receptor, i.e. potential therapeutic agonists and antagonists. XX SQ Sequence 265 AA: Query Match 99.1%; Score 1263; DB 23; Length 259; Best Local Similarity 99.2%; Pred. No. 4; e-122; Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 MYKKEKELFQFVPPVILVLDQDGNGKESVSGEKGDAYKTKLFLCTGKLPVWFL 60      :     :     :     :     :     :     :     : 1 MYKKEKELFQFVPPVILVLDQDGNGKESVSGEKGDAYKTKLFLCTGKLPVWFL 60	Db	1 MVSKEELFQFVPPVILVLDQDGNGKESVSGEKGDAYKTKLFLCTGKLPVWFL 60 1 MVSKEELFQFVPPVILVLDQDGNGKESVSGEKGDAYKTKLFLCTGKLPVWFL 60 61 LYTTISGVQCFSPRYDPHMKQHDFKFSAMPESVYQERTIFFKDGKNTKRAVEKEPDYL 120      :     :     :     :     :     :     : 61 LYTTISGVQCFSPRYDPHMKQHDFKFSAMPESVYQERTIFFKDGKNTKRAVEKEPDYL 120 Qy	61 LYTTISGVQCFSPRYDPHMKQHDFKFSAMPESVYQERTIFFKDGKNTKRAVEKEPDYL 120      :     :     :     :     :     : 61 LYTTISGVQCFSPRYDPHMKQHDFKFSAMPESVYQERTIFFKDGKNTKRAVEKEPDYL 120 Qy

Wed Jun 4 10:15:25 2003

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Db 61 LVTTLIYQOCFSRYPDHMKQHDFPKSAMPCYQBRTIFFKODGNYKTRAEVKFFGDTL 120  
Qy 121 VNRIELKGIDPREDGATLIGHLEYNSHNTYIMADKRGKIVNFKIRHNTIEGSVOLA 180  
Db 121 VNRIELKGIDPREDGATLIGHLEYNSHNTYIMADKRGKIVNFKIRHNTIEGSVOLA 180  
Qy 181 DHYQQTIPIGDCPVLLPDNHTLSTQSALSQPNKBDHNVILGFTTAFTTGLNDELYK 239  
Db 181 DHYQQTIPIGDCPVLLPDNHTLSTQSALSQPNKBDHNVILGFTTAFTTGLNDELYK 239

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